

SEQUENCE LISTING

BEST AVAILABLE COPY

<110> Bott, Richard R. Kellis, James T. Morrison, Thomas B.

<120> High Throughput Mutagenesis Screening Method

<130> GC724

<140> US 10/091,912

<141> 2002-03-05

<160> 2

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 818

<212> DNA

<213> Pseudomonas mendocina

<400> 1

tggcggcctc	ttgcctgtcc	gtctgtgcca	ctgtcgcggc	ggctcccctg	ccggatacac	60
cgggagcgcc	atttccggct	gtcgccaatt	tcgaccgcag	tggcccctac	accaccagca	120
gccagagcga	ggggccgagc	tgtcgcatct	atcggccccg	cgacctgggt	caggggggcg	180
tgcgtcatcc	ggtgattctc	tggggcaatg	gcaccggtgc	cgggccgtcc	acctatgccg	240
gcttgctatc	gcactgggca	agccacggtt	tcgtggtggc	ggcggcggaa	acctccaatg	300
ccggtaccgg	gcgggaaatg	ctcgcctgcc	tggactatct	ggtacgtgag	aacgacaccc	360
cctacggcac	ctattccggc	aagctcaata	ccgggcgagt	cggcacttct	gggcattccc	420
agggtggtgg	cggctcgatc	atggccgggc	aggatacgag	ggtgcgtacc	acggcgccga	480
tccagcccta	caccctcggc	ctggggcacg	acagcgcctc	gcagcggcgg	cagcaggggc	540
cgatgttcct	gatgtccggt	ggcggtgaca	ccatcgcctt	tccctacctc	aacgctcagc	600
	•	gtgccggtgt				660
tcgagccggt	cggtagcggt	ggggcctatc	gcggcccgag	cacggcatgg	ttccgcttcc	720
agctgatgga	tgaccaagac	gcccgcgcta	ccttctacgg	cgcgcagtgc	agtctgtgca	, 780 _. .
ccagcctgct	gtggtcggtc	gagcgccgcg	ggctttaa			818

<210> 2

<211> 272

<212> PRT

<213> Pseudomonas mendocina

<400> 2

Met
Ala
Ala
Ser
Cys
Leu
Ser
Val
Cys
Ala
Thr
Val
Ala
Ala
Ala
Pro
10
...
...
15
...
...
15
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...
...<

85 Glu Thr Ser Asn Ala Gly Thr Gly Arg Glu Met Leu Ala Cys Leu Asp 105 Tyr Leu Val Arg Glu Asn Asp Thr Pro Tyr Gly Thr Tyr Ser Gly Lys 120 Leu Asn Thr Gly Arg Val Gly Thr Ser Gly His Ser Gln Gly Gly 135 Gly Ser Ile Met Ala Gly Gln Asp Thr Arg Val Arg Thr Thr Ala Pro 150 155 Ile Gln Pro Tyr Thr Leu Gly Leu Gly His Asp Ser Ala Ser Gln Arg 170 Arg Gln Gln Gly Pro Met Phe Leu Met Ser Gly Gly Gly Asp Thr Ile 180 185 Ala Phe Pro Tyr Leu Asn Ala Gln Pro Val Tyr Arg Arg Ala Asn Val 200 205 Pro Val Phe Trp Gly Glu Arg Arg Tyr Val Ser His Phe Glu Pro Val 215 Gly Ser Gly Gly Ala Tyr Arg Gly Pro Ser Thr Ala Trp Phe Arg Phe 230 235 Gln Leu Met Asp Asp Gln Asp Ala Arg Ala Thr Phe Tyr Gly Ala Gln 245 250 Cys Ser Leu Cys Thr Ser Leu Leu Trp Ser Val Glu Arg Arg Gly Leu 265

BEST AVAILABLE COPY